

SEQUENCE LISTING

<110> Cohen, Dalia et al.

<120> Identification of Genes Involved in
Alzheimer's Disease Using Drosophila Melanogaster

<130> 4-31612 A

<150> 60/236,893

<151> 2000-09-29

<150> 60/298,309

<151> 2001-06-14

<160> 53

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<210> 1

<211> 123

<212> DNA

<213> Homo Sapien

<400> 1

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tag	123

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<212> DNA

<213> Homo Sapien

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atagcgtag	129

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<211> 300

<212> DNA

<213> Homo Sapien

<400> 3

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atagcgacag tgatcgatc cacttggtg atgctgaaga agaaacagta cacatccatt	180
catcatggtg tgggtggagg tgacgccgt gtcaccccag aggagcgcca cctgtccaag	240
atgcgcaga acggctacga aaatccaacc tacaagttct ttgagcagat gcagaactag	300

<210> 4

<211> 300
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 atagcgacag tgatcatcat caccttgggtg atgctgaaga agaaacagta cacatccatt 180
 catcatggtg tgggtggaggt tgacgccgct gtcaccccag aggagcgcca cctgtccaag 240
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<210> 5
 <211> 72
 <212> DNA
 <213> Homo Sapien

<400> 5
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 acagtgcagg ca 72

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 <211> 1537
 <212> DNA
 <213> Homo Sapien

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 gaattccacc caaggagcgg gcgcctggga tcagagcgtc ctgttttagca ataacggctg 180
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 gggctgcaga gatggagctt caggcaaaac ttacagctta accattttc aagcaaaaca 1140
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<210> 7
 <211> 332

<212> PRT

<213> Homo Sapien

<400> 7

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Gly Asp Val Arg Leu Ser Pro Val Ser Pro Leu Leu Ala Pro Pro Asp
35 40 45
Pro Arg Leu Ala Ser Arg Trp Glu Gly Arg Ser Arg Met Lys Gly Lys
50 55 60
Lys Gly Ile Val Ala Ala Ser Gly Ser Glu Thr Glu Asp Glu Asp Ser
65 70 75 80
Met Asp Ile Pro Leu Asp Leu Ser Ser Ser Ala Gly Ser Gly Lys Arg
85 90 95
Arg Arg Arg Gly Asn Leu Pro Lys Glu Ser Val Gln Ile Leu Arg Asp
100 105 110
Trp Leu Tyr Glu His Arg Tyr Asn Ala Tyr Pro Ser Glu Gln Glu Lys
115 120 125
Ala Leu Leu Ser Gln Gln Thr His Leu Ser Thr Leu Gln Val Cys Asn
130 135 140
Trp Phe Ile Asn Ala Arg Arg Arg Leu Leu Pro Asp Met Leu Arg Lys
145 150 155 160
Asp Gly Lys Asp Pro Asn Gln Phe Thr Ile Ser Arg Arg Gly Ala Lys
165 170 175
Ile Ser Glu Thr Ser Ser Val Glu Ser Val Met Gly Ile Lys Asn Phe
180 185 190
Met Pro Ala Leu Glu Glu Thr Pro Phe His Ser Cys Thr Ala Gly Pro
195 200 205
Asn Pro Thr Leu Gly Arg Pro Leu Ser Pro Lys Pro Ser Ser Pro Gly
210 215 220
Ser Val Leu Ala Arg Pro Ser Val Ile Cys His Thr Thr Val Thr Ala
225 230 235 240
Leu Lys Asp Val Pro Phe Ser Leu Cys Gln Ser Val Gly Val Gly Gln
245 250 255
Asn Thr Asp Ile Gln Gln Ile Ala Ala Lys Asn Phe Thr Asp Thr Ser
260 265 270
Leu Met Tyr Pro Glu Asp Thr Cys Lys Ser Gly Pro Ser Thr Asn Thr
275 280 285
Gln Ser Gly Leu Phe Asn Thr Pro Pro Pro Thr Pro Pro Asp Leu Asn
290 295 300
Gln Asp Phe Ser Gly Phe Gln Leu Leu Val Asp Val Ala Leu Lys Arg
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325 330

<210> 8

<211> 1053

<212> DNA

<213> Homo Sapien

<400> 8

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ccctcggccc	ccacaggccc	tgggcccctg	ctggagtttg	ctctgcacga	ggatctgctg	180
accctgtgtg	tgacatggca	gctgcaatgg	gatgagcttg	gggatggggg	cgaggaacgg	240
cgggctgagc	aactgaaact	atttgaaatg	ctagtgagcg	aagctcgcca	gccactgttg	300
cggcatgggc	cagttcgtga	ggctctgctc	accctgctgg	atgcctgtgg	ccgccctgtg	360
cccagtagcc	cagcactgga	tgaaggcttg	gtgctacttc	tcagccagct	gtgtgtttgt	420
gtggcccagg	agccttcatt	gctcgagtgc	ttctgcagc	cacctcctga	gcctggagcc	480
gctccccgtc	ttcttctctt	ttctgcctt	gtcccttttg	tgcacgaga	gggcaccctg	540
ggccagcagg	cccgatgatc	cctacttctt	ctcatggctt	tgtcagctgg	gagccccact	600
gtgggcccgt	acatcgcgga	tactctttac	ttctgcccgg	tgtggccac	agggctcagt	660
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atgatcgcca	gtaccgccta	cctggaactt	ttctacgga	gtatctcaga	gcctgctttg	960
ctccgtacct	tcctgcgatt	cctgttggtg	caccggcatg	acaccacac	catcctcgac	1020
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<210> 9
 <211> 351
 <212> PRT
 <213> Homo Sapien

<400> 9

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Leu	Leu	Ala	Glu	Asp	Arg	Ala	Val	Pro	Ser	Ala	Pro	Thr	Gly	Pro	Gly
		35					40					45			
Pro	Leu	Leu	Glu	Phe	Ala	Leu	His	Glu	Asp	Leu	Leu	Thr	Arg	Val	Leu
	50					55					60				
Thr	Trp	Gln	Leu	Gln	Trp	Asp	Glu	Leu	Gly	Asp	Gly	Val	Glu	Glu	Arg
65					70				75					80	
Arg	Ala	Glu	Gln	Leu	Lys	Leu	Phe	Glu	Met	Leu	Val	Ser	Glu	Ala	Arg
					85				90					95	
Gln	Pro	Leu	Leu	Arg	His	Gly	Pro	Val	Arg	Glu	Ala	Leu	Leu	Thr	Leu
			100					105					110		
Leu	Asp	Ala	Cys	Gly	Arg	Pro	Val	Pro	Ser	Ser	Pro	Ala	Leu	Asp	Glu
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Gly	Leu	Val	Leu	Leu	Leu	Ser	Gln	Leu	Cys	Val	Cys	Val	Ala	Gln	Glu
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Pro	Ser	Leu	Leu	Glu	Phe	Phe	Leu	Gln	Pro	Pro	Pro	Glu	Pro	Gly	Ala
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Ala	Pro	Arg	Leu	Leu	Leu	Phe	Ser	Arg	Leu	Val	Pro	Phe	Val	His	Arg
					165				170					175	
Glu	Gly	Thr	Leu	Gly	Gln	Gln	Ala	Arg	Asp	Ala	Leu	Leu	Leu	Leu	Met
			180					185					190		
Ala	Leu	Ser	Ala	Gly	Ser	Pro	Thr	Val	Gly	Arg	Tyr	Ile	Ala	Asp	His
		195					200					205			
Ser	Tyr	Phe	Cys	Pro	Val	Leu	Ala	Thr	Gly	Leu	Ser	Ala	Leu	Tyr	Ser
	210					215					220				
Ser	Leu	Pro	Arg	Lys	Ile	Glu	Val	Pro	Gly	Asp	Asp	Trp	His	Cys	Leu
225					230					235					240
Arg	Arg	Glu	Asp	Trp	Leu	Gly	Val	Pro	Ala	Leu	Ala	Leu	Phe	Met	Ser
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Ser Leu Glu Phe Cys Asn Ala Val Ile Gln Val Ala His Pro Leu Val
260 265 270
Gln Lys Gln Leu Val Asp Tyr Ile His Asn Gly Phe Leu Val Pro Val
275 280 285
Met Gly Pro Ala Leu His Lys Thr Ser Val Glu Glu Met Ile Ala Ser
290 295 300
Thr Ala Tyr Leu Glu Leu Phe Leu Arg Ser Ile Ser Glu Pro Ala Leu
305 310 315 320
Leu Arg Thr Phe Leu Arg Phe Leu Leu Leu His Arg His Asp Thr His
325 330 335
Thr Ile Leu Asp Thr Leu Val Ala Arg Ile Gly Ser Asn Ser Arg
340 345 350

<210> 10
<211> 1425
<212> DNA
<213> Homo Sapien

<400> 10
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gggccacact gatccgcata cctcttcata gagtccaacc tggacgcagg atcctgaacc 180
tactgagggg atggagagaa ccagcagagc tccccaagtt gggggcccca tcccctgggg 240
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<210> 11
<211> 433
<212> PRT
<213> Homo Sapien

<400> 11
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Pro Pro Leu Leu Gln Pro Leu Leu Leu Leu Pro Leu Leu Asn Val
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Glu Pro Ser Gly Ala Thr Leu Ile Arg Ile Pro Leu His Arg Val Gln

<213> Homo Sapien

<400> 12

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aaggatctca agctgatgaa aaaactggag cggcagcggg cacaggagga acaggcaaag    180
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<210> 13

<211> 381

<212> PRT

<213> Homo Sapien

<400> 13

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          20          25          30
Lys Lys Glu Glu Lys Lys Lys Trp Lys Asp Leu Lys Leu Met Lys Lys
          35          40          45
Leu Glu Arg Gln Arg Ala Gln Glu Glu Gln Ala Lys Arg Leu Glu Glu
          50          55          60
Glu Glu Ala Ala Ala Glu Lys Glu Asp Arg Gly Arg Pro Tyr Thr Leu
65          70          75          80
Ser Val Ala Leu Pro Gly Ser Ile Leu Asp Asn Ala Gln Ser Pro Glu
          85          90          95
Leu Arg Thr Tyr Leu Ala Gly Gln Ile Ala Arg Ala Cys Ala Ile Phe
          100          105          110
Cys Val Asp Glu Ile Val Val Phe Asp Glu Glu Gly Gln Asp Ala Lys
          115          120          125
Thr Val Glu Gly Glu Phe Thr Gly Val Gly Lys Lys Gly Gln Ala Cys
          130          135          140
Val Gln Leu Ala Arg Ile Leu Gln Tyr Leu Glu Cys Pro Gln Tyr Leu
          145          150          155          160
Arg Lys Ala Phe Phe Pro Lys His Gln Asp Leu Gln Phe Ala Gly Leu
          165          170          175
Leu Asn Pro Leu Asp Ser Pro His His Met Arg Gln Asp Glu Glu Ser
          180          185          190
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Glu Phe Arg	Glu Gly Ile Val Val	Asp Arg Pro Thr Arg Pro Gly His	
195	200	205	
Gly Ser Phe	Val Asn Cys Gly Met Lys Lys Glu Val Lys Ile Asp Lys		
210	215	220	
Asn Leu Glu	Pro Gly Leu Arg Val Thr Val Arg Leu Asn Gln Gln Gln		
225	230	235	240
His Pro Asp	Cys Lys Thr Tyr His Gly Lys Val Val Ser Ser Gln Asp		
	245	250	255
Pro Arg Thr	Lys Ala Gly Leu Tyr Trp Gly Tyr Thr Val Arg Leu Ala		
	260	265	270
Ser Cys Leu	Ser Ala Val Phe Ala Glu Ala Pro Phe Gln Asp Gly Tyr		
	275	280	285
Asp Leu Thr	Ile Gly Thr Ser Glu Arg Gly Ser Asp Val Ala Ser Ala		
	290	295	300
Gln Leu Pro	Asn Phe Arg His Ala Leu Val Val Phe Gly Gly Leu Gln		
305	310	315	320
Gly Leu Glu	Ala Gly Ala Asp Ala Asp Pro Asn Leu Glu Val Ala Glu		
	325	330	335
Pro Ser Val	Leu Phe Asp Leu Tyr Val Asn Thr Cys Pro Gly Gln Gly		
	340	345	350
Ser Arg Thr	Ile Arg Thr Glu Glu Ala Ile Leu Ile Ser Leu Ala Ala		
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Leu Gln Pro	Gly Leu Thr Gln Ala Gly Ala Arg His Thr		
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<210> 14

<211> 1779

<212> DNA

<213> Homo Sapien

<400> 14

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ccccaccac	gcgctgggac	tcagcagccg	ctaccacccc	tactccaaga	gcccgttcc	1680
cacgcctggc	gccccgtgc	cggtgcccgc	cgccaccgga	ccgtactact	ccccctacgc	1740
cctctacgga	cagagactga	ccaccgcctc	ggcgtgagg			1779

<210> 15

<211> 593

<212> PRT

<213> Homo Sapien

<400> 15

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			20					25					30		
Ala	Pro	Pro	Pro	Pro	Ala	Ala	Pro	Ala	Pro	Gly	Ala	Ser	Ala	Gln	Pro
			35					40				45			
Arg	Ala	Arg	Pro	Ala	Pro	Pro	Gly	Ala	Leu	Pro	Pro	Ala	Ala	Pro	Met
			50				55				60				
Arg	Ala	Gly	Ser	Ser	Pro	Ala	Gly	Ser	Thr	Lys	Pro	Phe	Val	His	Ala
65					70					75				80	
Val	Pro	Pro	Ser	Asp	Pro	Leu	Arg	Gln	Ala	Asn	Arg	Leu	Pro	Ile	Lys
				85					90					95	
Val	Leu	Lys	Met	Leu	Thr	Ala	Arg	Thr	Gly	His	Ile	Leu	His	Pro	Glu
			100					105					110		
Tyr	Leu	Gln	Pro	Leu	Pro	Ser	Thr	Pro	Val	Ser	Pro	Ile	Glu	Leu	Asp
			115				120					125			
Ala	Lys	Lys	Ser	Pro	Leu	Ala	Leu	Leu	Ala	Gln	Thr	Cys	Ser	Gln	Ile
			130				135				140				
Gly	Lys	Pro	Asp	Pro	Ser	Pro	Ser	Ser	Lys	Leu	Ser	Ser	Lys	Ser	Gly
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Phe	Arg	Val	Pro	Ser	Ala	Thr	Cys	Gln	Pro	Phe	Thr	Pro	Arg	Thr	Gly
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Ser	Pro	Ser	Ser	Ser	Ala	Ser	Ala	Cys	Ser	Pro	Gly	Gly	Met	Leu	Ser
			180					185					190		
Ser	Ala	Gly	Gly	Ala	Pro	Glu	Gly	Lys	Asp	Asp	Lys	Lys	Asp	Thr	Asp
			195				200					205			
Val	Gly	Gly	Gly	Gly	Lys	Gly	Thr	Gly	Gly	Ala	Ser	Ala	Glu	Gly	Gly
			210				215					220			
Pro	Thr	Gly	Leu	Ala	His	Gly	Arg	Ile	Ser	Cys	Gly	Gly	Gly	Ile	Asn
225					230					235					240
Val	Asp	Val	Asn	Gln	His	Pro	Asp	Gly	Gly	Pro	Gly	Gly	Lys	Ala	Leu
				245					250					255	
Gly	Ser	Asp	Cys	Gly	Gly	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Ser	Gly	Pro
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Ser	Ala	Pro	Thr	Ser	Ser	Ser	Val	Leu	Gly	Ser	Gly	Leu	Val	Ala	Pro
			275				280					285			
Val	Ser	Pro	Tyr	Lys	Pro	Gly	Gln	Thr	Val	Phe	Pro	Leu	Pro	Pro	Ala
			290				295					300			
Gly	Met	Thr	Tyr	Pro	Gly	Ser	Leu	Ala	Gly	Ala	Tyr	Ala	Gly	Tyr	Pro
305					310					315					320
Pro	Gln	Phe	Leu	Pro	His	Gly	Val	Ala	Leu	Asp	Pro	Thr	Lys	Pro	Gly
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Ser Leu Val Gly Ala Gln Leu Ala Ala Ala Ala Gly Ser Leu Gly
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Cys Ser Lys Pro Ala Gly Ser Ser Pro Leu Ala Gly Ala Ser Pro Pro
355 360 365
Ser Val Met Thr Ala Ser Leu Cys Arg Asp Pro Tyr Cys Leu Ser Tyr
370 375 380
His Cys Ala Ser His Leu Ala Gly Ala Ala Ala Ala Ser Ala Ser Cys
385 390 395 400
Ala His Asp Pro Ala Ala Ala Ala Ala Leu Lys Ser Gly Tyr Pro
405 410 415
Leu Val Tyr Pro Thr His Pro Leu His Gly Val His Ser Ser Leu Thr
420 425 430
Ala Ala Ala Ala Ala Gly Ala Thr Pro Pro Ser Leu Ala Gly His Pro
435 440 445
Leu Tyr Pro Tyr Gly Phe Met Leu Pro Asn Asp Pro Leu Pro His Ile
450 455 460
Cys Asn Trp Val Ser Ala Asn Gly Pro Cys Asp Lys Arg Phe Ala Thr
465 470 475 480
Ser Glu Glu Leu Leu Ser His Leu Arg Thr His Thr Ala Phe Pro Gly
485 490 495
Thr Asp Lys Leu Leu Ser Gly Tyr Pro Ser Ser Ser Ser Met Ala Ser
500 505 510
Ala Ala Ala Ala Ala Met Ala Cys His Met His Ile Pro Thr Ser Gly
515 520 525
Ala Pro Gly Ser Pro Gly Asp Ala Gly Ala Ala Gln Pro Pro Pro Arg
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Ala Gly Thr Gln Gln Pro Leu Pro Pro Leu Leu Gln Glu Pro Ala Ser
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<210> 16
<211> 1938
<212> DNA
<213> Homo Sapien

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cggcactccc gcagtccagc cggctcctct agcccggcca cggctccgct gcggggccacc 180
caggattact cgcgtctggc tccaggcgcc gagaaggcgc gctgggcgcc cgtggccgcc 240
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taccaccctt actccaagag cccgcttccc acgctggcg ccccggtgcc ggtgcccgc 1860
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<210> 17
<211> 645
<212> PRT
<213> Homo Sapien

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<400> 17
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Pro Arg Arg Thr Pro Arg Ala Ala Arg His Ser Arg Ser Pro Ala Gly
          35          40          45
Ser Ser Ser Pro Ala Thr Ala Pro Leu Arg Ala Thr Gln Asp Tyr Ser
          50          55          60
Arg Leu Ala Pro Gly Ala Glu Lys Ala Arg Trp Ala Pro Val Ala Ala
          65          70          75          80
Ala Pro Ala Pro Pro Pro Pro Ala Ala Pro Ala Pro Gly Ala Ser Ala
          85          90          95
Gln Pro Arg Ala Arg Pro Ala Pro Pro Gly Ala Leu Pro Pro Ala Ala
          100          105          110
Pro Met Arg Ala Gly Ser Ser Pro Ala Gly Ser Thr Lys Pro Phe Val
          115          120          125
His Ala Val Pro Pro Ser Asp Pro Leu Arg Gln Ala Asn Arg Leu Pro
          130          135          140
Ile Lys Val Leu Lys Met Leu Thr Ala Arg Thr Gly His Ile Leu His
          145          150          155          160
Pro Glu Tyr Leu Gln Pro Leu Pro Ser Thr Pro Val Ser Pro Ile Glu
          165          170          175
Leu Asp Ala Lys Lys Ser Pro Leu Ala Leu Leu Ala Gln Thr Cys Ser
          180          185          190
Gln Ile Gly Lys Pro Asp Pro Ser Pro Ser Ser Lys Leu Ser Ser Lys
          195          200          205
Ser Gly Phe Arg Val Pro Ser Ala Thr Cys Gln Pro Phe Thr Pro Arg
          210          215          220
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<211> 4022
 <212> DNA
 <213> Homo Sapien

<220>
 <221> misc_feature
 <222> (1)...(4022)
 <223> n = A,T,C or G

<400> 18

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<210> 19

<211> 1265

<212> PRT

<213> Homo Sapien

<220>

<221> VARIANT

<222> (1)...(1265)

<223> Xaa = Any Amino Acid

<400> 19

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      20             25             30
His His Arg Gly Glu Xaa Xaa Arg Arg Gln Glu Glu Ala Ala Leu Leu
      35             40             45
Ser Gln Glu Phe Ala Glu Ala Trp Gly Gln Lys Ala Lys Glu Leu Tyr
      50             55             60
Glu Pro Ile Trp Gln Asn Phe Thr Asp Pro Gln Leu Arg Arg Ile Ile
      65             70             75             80
Gly Ala Val Arg Thr Leu Gly Ser Ala Asn Leu Pro Leu Ala Lys Arg
      85             90             95
Gln Gln Tyr Asn Ala Leu Leu Ser Asn Met Ser Arg Ile Tyr Ser Thr
      100            105            110
Ala Lys Val Cys Leu Pro Asn Lys Thr Ala Thr Cys Trp Ser Leu Asp
      115            120            125
Pro Asp Leu Thr Asn Ile Leu Ala Ser Ser Arg Ser Tyr Ala Met Leu
      130            135            140
Leu Phe Ala Trp Glu Gly Trp His Asn Ala Ala Gly Ile Pro Leu Lys
      145            150            155            160

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Pro	Thr	Phe	Glu	Asp	Asp	Leu	Glu	His	Leu	Tyr	Gln	Gln	Leu	Glu	Pro	195	200	205
Leu	Tyr	Leu	Asn	Leu	His	Ala	Phe	Val	Arg	Arg	Ala	Leu	His	Arg	Arg	210	215	220
Tyr	Gly	Asp	Arg	Tyr	Ile	Asn	Leu	Arg	Gly	Pro	Ile	Pro	Ala	His	Leu	225	230	235
Leu	Gly	Asp	Met	Trp	Ala	Gln	Ser	Trp	Glu	Asn	Ile	Tyr	Asp	Met	Val	245	250	255
Val	Pro	Phe	Pro	Asp	Lys	Pro	Asn	Leu	Asp	Val	Thr	Ser	Thr	Met	Leu	260	265	270
Gln	Gln	Gly	Trp	Asn	Ala	Thr	His	Met	Phe	Arg	Val	Ala	Glu	Glu	Phe	275	280	285
Phe	Thr	Ser	Leu	Glu	Leu	Ser	Pro	Met	Pro	Pro	Glu	Phe	Trp	Glu	Gly	290	295	300
Ser	Met	Leu	Glu	Lys	Pro	Ala	Asp	Gly	Arg	Glu	Val	Val	Cys	His	Ala	305	310	315
Ser	Ala	Trp	Asp	Phe	Tyr	Asn	Arg	Lys	Asp	Phe	Arg	Ile	Lys	Gln	Cys	325	330	335
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His	Ile	Gln	Tyr	Tyr	Leu	Gln	Tyr	Lys	Asp	Leu	Pro	Val	Ser	Leu	Arg	355	360	365
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Arg	Val	Thr	Asn	Asp	Thr	Glu	Ser	Asp	Ile	Asn	Tyr	Leu	Leu	Lys	Met	405	410	415
Ala	Leu	Glu	Lys	Ile	Ala	Phe	Leu	Pro	Phe	Gly	Tyr	Leu	Val	Asp	Gln	420	425	430
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Phe	Asp	Trp	Trp	Tyr	Leu	Arg	Thr	Lys	Tyr	Gln	Gly	Ile	Cys	Pro	Pro	450	455	460
Val	Thr	Arg	Asn	Glu	Thr	His	Phe	Asp	Ala	Gly	Ala	Lys	Phe	His	Val	465	470	475
Pro	Asn	Val	Thr	Pro	Tyr	Ile	Arg	Tyr	Phe	Val	Ser	Phe	Val	Leu	Gln	485	490	495
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Leu	His	Gln	Cys	Asp	Ile	Tyr	Arg	Ser	Thr	Lys	Ala	Gly	Ala	Lys	Leu	515	520	525
Arg	Lys	Val	Leu	Gln	Ala	Gly	Ser	Ser	Arg	Pro	Trp	Gln	Glu	Val	Leu	530	535	540
Lys	Asp	Met	Val	Gly	Leu	Asp	Ala	Leu	Asp	Ala	Gln	Pro	Leu	Leu	Lys	545	550	555
Tyr	Phe	Gln	Pro	Val	Thr	Gln	Trp	Leu	Gln	Glu	Gln	Asn	Gln	Gln	Asn	565	570	575
Gly	Glu	Val	Leu	Gly	Trp	Pro	Glu	Tyr	Gln	Trp	His	Pro	Pro	Leu	Pro	580	585	590
Asp	Asn	Tyr	Pro	Glu	Gly	Ile	Asp	Leu	Val	Thr	Asp	Glu	Ala	Glu	Ala			

Thr Lys Glu Asn Tyr Asn Gln Glu Trp Trp Ser Leu Arg Leu Lys Tyr
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 Gln Gly Leu Cys Pro Pro Val Pro Arg Thr Gln Gly Asp Phe Asp Pro
 1060 1065 1070
 Gly Ala Lys Phe His Ile Pro Ser Ser Val Pro Tyr Ile Arg Tyr Phe
 1075 1080 1085
 Val Ser Phe Ile Ile Gln Phe Gln Phe His Glu Ala Leu Cys Gln Ala
 1090 1095 1100
 Ala Gly His Thr Gly Pro Leu His Lys Cys Asp Ile Tyr Gln Ser Lys
 1105 1110 1115 1120
 Glu Ala Gly Gln Arg Leu Ala Thr Ala Met Lys Leu Gly Phe Ser Arg
 1125 1130 1135
 Pro Trp Pro Glu Ala Met Gln Leu Ile Thr Gly Gln Pro Asn Met Ser
 1140 1145 1150
 Ala Ser Ala Met Leu Ser Tyr Phe Lys Pro Leu Leu Asp Trp Leu Arg
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 Thr Glu Asn Glu Leu His Gly Glu Lys Leu Gly Trp Pro Gln Tyr Asn
 1170 1175 1180
 Trp Thr Pro Asn Ser Ala Arg Ser Glu Gly Pro Leu Pro Asp Ser Gly
 1185 1190 1195 1200
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 Gly Gln Trp Leu Leu Leu Phe Leu Gly Ile Ala Leu Leu Val Ala Thr
 1220 1225 1230
 Leu Gly Leu Ser Gln Arg Leu Phe Ser Ile Arg His Arg Ser Leu His
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 Ser
 1265

<210> 20
 <211> 954
 <212> DNA
 <213> Homo Sapien

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<210> 21

<211> 288
 <212> PRT
 <213> Homo Sapien

<400> 21

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			20					25					30		
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Val	Leu	Val	His	Thr	Thr	Leu	Pro	Ser	Gln	Glu	Val	Gln	Ala	Leu	Leu
65					70					75					80
Glu	Gly	Thr	Gly	Arg	Gln	Ala	Val	Leu	Lys	Gly	Met	Gly	Ser	Gly	Gln
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Leu	Gln	Asn	Leu	Gly	Ala	Ala	Val	Ala	Ile	Leu	Gly	Gly	Pro	Gly	Thr
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Val	Gln	Gly	Val	Val	Arg	Phe	Leu	Gln	Leu	Thr	Pro	Glu	Arg	Cys	Leu
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Ile	Glu	Gly	Thr	Ile	Asp	Gly	Leu	Glu	Pro	Gly	Leu	His	Gly	Leu	His
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Val	His	Gln	Tyr	Gly	Asp	Leu	Thr	Asn	Asn	Cys	Asn	Ser	Cys	Gly	Asn
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His	Phe	Asn	Pro	Asp	Gly	Ala	Ser	His	Gly	Gly	Pro	Gln	Asp	Ser	Asp
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Arg	His	Arg	Gly	Asp	Leu	Gly	Asn	Val	Arg	Ala	Asp	Ala	Asp	Gly	Arg
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Ala	Ile	Phe	Arg	Met	Glu	Asp	Glu	Gln	Leu	Lys	Val	Trp	Asp	Val	Ile
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225					230					235					240
Cys	Gly	Ile	Ile	Ala	Arg	Ser	Ala	Gly	Leu	Phe	Gln	Asn	Pro	Lys	Gln
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Ile	Cys	Ser	Cys	Asp	Gly	Leu	Thr	Ile	Trp	Glu	Glu	Arg	Gly	Arg	Pro
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<210> 22
 <211> 1006
 <212> DNA
 <213> Homo Sapien

<400> 22

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<210> 23
<211> 240
<212> PRT
<213> Homo Sapien

<400> 23
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35 40 45
Asn Pro Leu Lys Lys Val Pro Ala Leu Lys Asp Gly Asp Phe Thr Leu
50 55 60
Thr Glu Ser Val Ala Ile Leu Leu Tyr Leu Thr Arg Lys Tyr Lys Val
65 70 75 80
Pro Asp Tyr Trp Tyr Pro Gln Asp Leu Gln Ala Arg Ala Arg Val Asp
85 90 95
Glu Tyr Leu Ala Trp Gln His Thr Thr Leu Arg Arg Ser Cys Leu Arg
100 105 110
Ala Leu Trp His Lys Val Met Phe Pro Val Phe Leu Gly Glu Pro Val
115 120 125
Ser Pro Gln Thr Leu Ala Ala Thr Leu Ala Glu Leu Asp Val Thr Leu
130 135 140
Gln Leu Leu Glu Asp Lys Phe Leu Gln Asn Lys Ala Phe Leu Thr Gly
145 150 155 160
Pro His Ile Ser Leu Ala Asp Leu Val Ala Ile Thr Glu Leu Met His
165 170 175
Pro Val Gly Ala Gly Cys Gln Val Phe Glu Gly Arg Pro Lys Leu Ala
180 185 190
Thr Trp Arg Gln Arg Val Glu Ala Ala Val Gly Glu Asp Leu Phe Gln
195 200 205
Glu Ala His Glu Val Ile Leu Lys Ala Lys Asp Phe Pro Pro Ala Asp
210 215 220
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225 230 235 240

<210> 24
<211> 2442
<212> DNA
<213> Homo Sapien

<400> 24
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<210> 25
 <211> 813
 <212> PRT
 <213> Homo Sapien

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 Arg Val Leu Ala Ser Asp Ala Ala Phe Leu Lys Lys Ser Gly Leu
 35 40 45
 Pro Asp Leu Ile Leu Gly Lys Ile Trp Asp Leu Ala Asp Thr Asp Gly
 50 55 60

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Glu Met Lys Asp Leu Glu Asn His Asn Ser Gln Leu Asn Trp Cys Ser					
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Ser Pro His Ser Ile Leu Val Asn Gly Ala Thr Asp Tyr Cys Ser Leu					
530		535		540	
Ser Thr Ser Ser Ser Glu Thr Ala Asn Leu Asn Glu His Val Glu Gly					
545		550		555	560
Gln Ser Asn Leu Glu Ser Glu Pro Ile His Gln Glu Ser Pro Ser Asp					
565		570		575	
Pro Phe Val Gly Asn Pro Phe Gly Gly Asp Pro Phe Lys Gly Ser Asp					
580		585		590	
Pro Phe Ala Ser Asp Cys Phe Phe Arg Gln Ser Thr Asp Pro Phe Ala					
595		600		605	
Thr Ser Ser Thr Asp Pro Phe Ser Ala Ala Asn Asn Ser Ser Ile Thr					
610		615		620	
Ser Val Glu Thr Leu Lys His Asn Asp Pro Phe Ala Pro Gly Gly Thr					
625		630		635	640
Val Val Ala Ala Ser Asp Ser Ala Thr Asp Pro Phe Ala Ser Val Phe					
645		650		655	
Gly Asn Glu Ser Phe Gly Gly Gly Phe Ala Asp Phe Ser Thr Leu Ser					
660		665		670	
Lys Val Asn Asn Glu Asp Pro Phe Arg Ser Ala Thr Ser Ser Ser Val					
675		680		685	
Ser Asn Val Val Ile Thr Lys Asn Val Phe Glu Glu Thr Ser Val Lys					
690		695		700	
Ser Glu Asp Glu Pro Pro Ala Leu Pro Pro Lys Ile Gly Thr Pro Thr					
705		710		715	720
Arg Pro Cys Pro Leu Pro Pro Gly Asn Asp Ser Pro Lys Glu Lys Asp					
725		730		735	
Pro Glu Met Phe Cys Asp Pro Phe Thr Ser Ala Thr Thr Thr Thr Asn					
740		745		750	
Lys Glu Ala Asp Pro Ser Asn Phe Ala Asn Phe Ser Ala Tyr Pro Ser					
755		760		765	
Glu Glu Asp Met Ile Glu Trp Ala Lys Arg Glu Ser Glu Arg Glu Glu					
770		775		780	
Glu Gln Arg Leu Ala Arg Leu Asn Gln Gln Glu Gln Glu Asp Leu Glu					
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<210> 26
 <211> 1357
 <212> DNA
 <213> Homo Sapien

<400> 26

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aggccccatg	tggatttctt	cctggaagtg	gtgagccagt	ggtacgagct	ggtgggtgtt	420
acagcaagca	tggagatcta	tggctctgct	gtggcagata	aactggacaa	tagcagaagc	480
attcttaaga	ggagatatta	cagacagcac	tgcacttttg	agttgggcag	ctacatcaag	540

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<210> 27
 <211> 254
 <212> PRT
 <213> Homo Sapien

<400> 27

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20          25          30
Phe Phe Ile Tyr Leu Leu Arg Arg Gln Ile Arg Thr Val Ile Gln Tyr
35          40          45
Gln Thr Val Arg Tyr Asp Ile Leu Pro Leu Ser Pro Val Ser Arg Asn
50          55          60
Arg Leu Ala Gln Val Lys Arg Lys Ile Leu Val Leu Asp Leu Asp Glu
65          70          75          80
Thr Leu Ile His Ser His His Asp Gly Val Leu Arg Pro Thr Val Arg
85          90          95
Pro Gly Thr Pro Pro Asp Phe Ile Leu Lys Val Val Ile Asp Lys His
100          105          110
Pro Val Arg Phe Phe Val His Lys Arg Pro His Val Asp Phe Phe Leu
115          120          125
Glu Val Val Ser Gln Trp Tyr Glu Leu Val Val Phe Thr Ala Ser Met
130          135          140
Glu Ile Tyr Gly Ser Ala Val Ala Asp Lys Leu Asp Asn Ser Arg Ser
145          150          155          160
Ile Leu Lys Arg Arg Tyr Tyr Arg Gln His Cys Thr Leu Glu Leu Gly
165          170          175
Ser Tyr Ile Lys Asp Leu Ser Val Val His Ser Asp Leu Ser Ser Ile
180          185          190
Val Ile Leu Asp Asn Ser Pro Gly Ala Tyr Arg Ser His Pro Asp Asn
195          200          205
Ala Ile Pro Ile Lys Ser Trp Phe Ser Asp Pro Ser Asp Thr Ala Leu
210          215          220
Leu Asn Leu Leu Pro Met Leu Asp Ala Leu Arg Phe Thr Ala Asp Val
225          230          235          240
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<210> 28

<211> 1812
 <212> DNA
 <213> Homo Sapien

<400> 28

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<210> 29
 <211> 603
 <212> PRT
 <213> Homo Sapien

<400> 29

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			20					25					30		
Cys	Lys	Gln	Ile	Leu	Ser	Asn	Pro	Lys	Phe	Ala	Glu	His	Gly	Gly	Trp
		35					40				45				
His	Val	Tyr	Gly	Leu	Leu	Gln	Arg	Ser	Asp	Lys	Lys	Tyr	Asp	Glu	Ala
	50					55				60					
Ile	Lys	Cys	Tyr	Arg	Asn	Ala	Leu	Lys	Trp	Asp	Lys	Asp	Asn	Leu	Gln
65				70				75					80		
Ile	Leu	Arg	Asp	Leu	Ser	Leu	Leu	Gln	Ile	Gln	Met	Arg	Asp	Leu	Glu
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 Ser Ala Glu Ala Glu Glu Leu Ala Asn Glu Ile
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<210> 30
 <211> 1351
 <212> DNA
 <213> Homo Sapien

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<210> 32
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<400> 32

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CCDS:3750.1 Homo sapiens

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<211> 488

<212> PRT

<213> Homo Sapien

<400> 35

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<210> 38
 <211> 2404
 <212> DNA
 <213> Homo Sapien

<400> 38

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 <211> 278
 <212> PRT
 <213> Homo Sapien

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 Leu Ala Arg Ala Gly Phe Tyr Ala Leu Gly Glu Gly Asp Lys Val Lys
 65 70 75 80
 Cys Phe His Cys Gly Gly Gly Leu Thr Asp Trp Lys Pro Ser Glu Asp
 85 90 95
 Pro Trp Glu Gln His Ala Lys Trp Tyr Pro Gly Cys Lys Tyr Leu Leu
 100 105 110
 Glu Gln Lys Gly Gln Glu Tyr Ile Asn Asn Ile His Leu Thr His Ser
 115 120 125
 Leu Glu Glu Cys Leu Val Arg Thr Thr Glu Lys Thr Pro Ser Leu Thr
 130 135 140
 Arg Arg Ile Asp Asp Thr Ile Phe Gln Asn Pro Met Val Gln Glu Ala
 145 150 155 160
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 165 170 175
 Lys Ile Gln Ile Ser Gly Ser Asn Tyr Lys Ser Leu Glu Val Leu Val
 180 185 190
 Ala Asp Leu Val Asn Ala Gln Lys Asp Ser Met Gln Asp Glu Ser Ser
 195 200 205
 Gln Thr Ser Leu Gln Lys Glu Ile Ser Thr Glu Glu Gln Leu Arg Arg
 210 215 220
 Leu Gln Glu Glu Lys Leu Cys Lys Ile Cys Met Asp Arg Asn Ile Ala
 225 230 235 240
 Ile Val Phe Val Pro Cys Gly His Leu Val Thr Cys Lys Gln Cys Ala
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<210> 40
 <211> 2409
 <212> DNA
 <213> Homo Sapien

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His	Gly	Ala	Asp	Pro	Asn	Ala	Arg	Asp	Asn	Trp	Asn	Tyr	Thr	Pro
			115					120					125	Leu
His	Glu	Ala	Ala	Ile	Lys	Gly	Lys	Ile	Asp	Val	Cys	Ile	Val	Leu
			130					135				140		Leu
Gln	His	Gly	Ala	Glu	Pro	Thr	Ile	Arg	Asn	Thr	Asp	Gly	Arg	Thr
145											155			160
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Val	Tyr	Ser	Gly	Tyr	Ser	Arg	Lys	Pro	Val	Lys	Asn	Asn	Leu	Ala
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Ser	Gly	Asn	Glu	Glu	Lys	Met	Met	Ala	Leu	Leu	Thr	Pro	Leu	Asn
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Asn	Cys	His	Ala	Ser	Asp	Gly	Arg	Lys	His	Gly	Ala	Cys	Val	Asn
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Met	Asp	Leu	Trp	Gln	Phe	Thr	Pro	Leu	His	Glu	Ala	Ala	Ser	Lys
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Arg	Val	Glu	Val	Cys	Ser	Leu	Leu	Leu	Ser	Tyr	Gly	Ala	Asp	Pro
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Leu	Leu	Asn	Cys	His	Asn	Lys	Ser	Ala	Ile	Asp	Leu	Ala	Pro	Thr
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Gln	Leu	Lys	Glu	Arg	Leu	Ala	Tyr	Glu	Phe	Lys	Gly	His	Ser	Leu
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Gln	Ala	Ala	Arg	Glu	Ala	Asp	Val	Thr	Arg	Ile	Lys	Lys	His	Leu
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Leu	Glu	Met	Val	Asn	Phe	Lys	His	Pro	Gln	Thr	His	Glu	Thr	Ala
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Lys	Leu	Cys	Thr	Val	Gln	Ser	Val	Asn	Cys	Arg	Asp	Ile	Glu	Gly
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Gln	Ser	Thr	Pro	Leu	His	Phe	Ala	Ala	Gly	Tyr	Asn	Arg	Val	Ser
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Val	Glu	Tyr	Leu	Leu	Gln	His	Gly	Ala	Asp	Val	His	Ala	Lys	Asp
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Gly	Gly	Leu	Val	Pro	Leu	His	Asn	Ala	Cys	Ser	Tyr	Gly	His	Tyr
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Val	Ala	Glu	Leu	Leu	Val	Lys	His	Gly	Ala	Val	Val	Asn	Val	Ala
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Leu	Trp	Lys	Phe	Thr	Pro	Leu	His	Glu	Ala	Ala	Ala	Lys	Gly	Lys
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Glu	Ile	Cys	Lys	Leu	Leu	Leu	Gln	His	Gly	Ala	Asp	Pro	Thr	Lys
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Asn	Arg	Asp	Gly	Asn	Thr	Pro	Leu	Asp	Leu	Val	Lys	Asp	Gly	Asp
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Asp	Ile	Gln	Asp	Leu	Leu	Arg	Gly	Asp	Ala	Ala	Leu	Leu	Asp	Ala
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Val	Asn	Cys												

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Asp	Leu	Ser	Pro	Asp	Asp	Lys	Glu	Phe	Gln	Ser	Val	Glu	Glu	Glu	Met
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Gln	Ser	Thr	Val	Arg	Glu	His	Arg	Asp	Gly	Gly	His	Ala	Gly	Gly	Ile
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Lys	Asp	Arg	Ser	Cys	Tyr	Ile	Cys	His	Arg	Gln	Leu	Leu	Phe	Cys	Arg
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Val	Thr	Leu	Gly	Lys	Ser	Phe	Leu	Gln	Phe	Ser	Ala	Met	Lys	Met	Ala
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<212> DNA
<213> Homo Sapien
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 <213> Homo Sapien

<400> 43

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Glu	Lys	Ala	Leu	Asp	Tyr	Ile	Lys	Asn	Gly	Val	Asp	Ile	Asn	Ile	Cys
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Asn	Gln	Asn	Gly	Leu	Asn	Ala	Leu	His	Leu	Ala	Ser	Lys	Glu	Gly	His
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Val	Glu	Val	Val	Ser	Glu	Leu	Leu	Gln	Arg	Glu	Ala	Asn	Val	Asp	Ala
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Ala	Thr	Lys	Lys	Gly	Asn	Thr	Ala	Leu	His	Ile	Ala	Ser	Leu	Ala	Gly
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Gln	Ala	Glu	Val	Val	Lys	Val	Leu	Val	Thr	Asn	Gly	Ala	Asn	Val	Asn
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Ala	Gln	Ser	Gln	Asn	Gly	Phe	Thr	Pro	Leu	Tyr	Met	Ala	Ala	Gln	Glu
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Ser	Leu	Ala	Thr	Glu	Asp	Gly	Phe	Thr	Pro	Leu	Ala	Val	Ala	Leu	Gln
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Gln	Gly	His	Asp	Gln	Val	Val	Ser	Leu	Leu	Leu	Glu	Asn	Asp	Thr	Lys
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Gly	Lys	Val	Arg	Leu	Pro	Ala	Leu	His	Ile	Ala	Ala	Arg	Lys	Asp	Asp
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Thr	Lys	Ala	Ala	Ala	Leu	Leu	Leu	Gln	Asn	Asp	Asn	Asn	Ala	Asp	Val
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Glu	Ser	Lys	Ser	Gly	Phe	Thr	Pro	Leu	His	Ile	Ala	Ala	His	Tyr	Gly
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Asn	Ile	Asn	Val	Ala	Thr	Leu	Leu	Leu	Asn	Arg	Ala	Ala	Ala	Val	Asp

Thr	His	Ile	Ile	Asn	Val	Leu	Leu	Gln	Asn	Asn	Ala	Ser	Pro	Asn	Glu
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Leu	Thr	Val	Thr	Val	Thr	Glu	Lys	His	Lys	Met	Asn	Val	Pro	Glu	Thr
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Met	Asn	Glu	Val	Leu	Asp	Met	Ser	Asp	Asp	Glu	Val	Arg	Lys	Ala	Asn
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Ala	Pro	Glu	Met	Leu	Ser	Asp	Gly	Glu	Tyr	Ile	Ser	Asp	Val	Glu	Glu
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Gly	Asn	Arg	Cys	Thr	Trp	Tyr	Lys	Ile	Pro	Lys	Val	Gln	Glu	Phe	Thr
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Val	Lys	Thr	Asp	Thr	Phe	Lys	Arg	Glu	Ala	Phe	Asp	Val	Gly	Leu	Leu
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Ser	Thr	Ser	Ala	Gly	Glu	Asp	Ala	Met	Thr	Gly	Asp	Thr	Asp	Lys	Tyr
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Leu	Gly	Pro	Gln	Asp	Leu	Lys	Glu	Leu	Gly	Asp	Asp	Ser	Leu	Pro	Ala
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Glu	Gly	Tyr	Met	Gly	Phe	Ser	Leu	Gly	Ala	Arg	Ser	Ala	Arg	Phe	Leu
785						790				795					800
Val	Ser	Phe	Met	Val	Asp	Ala	Arg	Gly	Gly	Ser	Met	Arg	Gly	Ser	Arg
				805					810					815	
His	His	Gly	Met	Arg	Ile	Ile	Ile	Pro	Pro	Arg	Lys	Cys	Thr	Ala	Pro
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Thr	Arg	Ile	Thr	Cys	Arg	Leu	Val	Lys	Arg	His	Lys	Leu	Ala	Asn	Pro
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Pro	Pro	Met	Val	Glu	Gly	Glu	Gly	Leu	Ala	Ser	Arg	Leu	Val	Glu	Met
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His	Phe	Gly	Ser	Met	Arg	Gly	Lys	Glu	Arg	Glu	Leu	Ile	Val	Leu	Arg
				885					890					895	
Ser	Glu	Asn	Gly	Glu	Thr	Trp	Lys	Glu	His	Gln	Phe	Asp	Ser	Lys	Asn
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Glu	Asp	Leu	Thr	Glu	Leu	Leu	Asn	Gly	Met	Asp	Glu	Glu	Leu	Asp	Ser
			915					920					925		
Pro	Glu	Glu	Leu	Gly	Lys	Lys	Arg	Ile	Cys	Arg	Ile	Ile	Thr	Lys	Asp
			930				935					940			
Phe	Pro	Gln	Tyr	Phe	Ala	Val	Val	Ser	Arg	Ile	Lys	Gln	Glu	Ser	Asn
945						950				955					960
Gln	Ile	Gly	Pro	Glu	Gly	Gly	Ile	Leu	Ser	Ser	Thr	Thr	Val	Pro	Leu
				965					970					975	
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Gly	Leu	Gln	Ala	Gln	Pro	Val	Pro	Asp	Glu	Ile	Val	Lys	Lys	Ile	Leu
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Gly	Asn	Lys	Ala	Thr</											

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Leu Ala Pro Leu Thr Lys Gly Gly Gln Gln Leu Val Phe Asn Phe Tyr		
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Ser Phe Lys Glu Asn Arg Leu Pro Phe Ser Ile Lys Ile Arg Asp Thr		
1140	1145	1150
Ser Gln Glu Pro Cys Gly Arg Leu Ser Phe Leu Lys Glu Pro Lys Thr		
1155	1160	1165
Thr Lys Gly Leu Pro Gln Thr Ala Val Cys Asn Leu Asn Ile Thr Leu		
1170	1175	1180
Pro Ala His Lys Lys Ile Glu Lys Thr Asp Arg Arg Gln Ser Phe Ala		
1185	1190	1195 1200
Ser Leu Ala Leu Arg Lys Arg Tyr Ser Tyr Leu Thr Glu Pro Gly Met		
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Lys Glu Lys Lys Met Gln Ser Glu Leu Ser Asp Glu Glu Glu Ser Thr		
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Ser Arg Asn Thr Ser Leu Ser Glu Thr Ser Arg Gly Gly Gln Pro Ser		
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Val Thr Thr Lys Ser Ala Arg Asp Lys Lys Thr Glu Ala Ala Pro Leu		
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Lys Ser Lys Ser Glu Lys Ala Gly Ser Glu Lys Arg Ser Ser Arg Arg		
1265	1270	1275 1280
Thr Ala Asp Ala Leu Thr Ser Val Leu Thr Lys Ile Asn Arg Ile Asp		
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Ile Val Thr Leu Leu Glu Gly Pro Ile Phe Asp Tyr Gly Asn Ile Ser		
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Gly Thr Arg Ser Phe Ala Asp Glu Asn Asn Val Phe His Asp Pro Val		
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Asp Gly Tyr Pro Ser Leu Gln Val Glu Leu Glu Thr Pro Thr Gly Leu		
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His Tyr Thr Pro Pro Thr Pro Phe Gln Gln Asp Asp Tyr Phe Ser Asp		
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Gly Leu Val Pro Ser Gln Gly Asn Ile Glu His Ser Ala Asp Gly Pro		
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Pro Val Val Thr Ala Glu Asp Ala Ser Leu Glu Asp Ser Lys Leu Glu		
1395	1400	1405
Asp Ser Val Pro Leu Thr Glu Met Pro Glu Ala Val Asp Val Asp Glu		
1410	1415	1420
Ser Gln Leu Glu Asn Val Cys Leu Ser Glu Tyr Pro Gln Tyr Leu Gly		
1425	1430	1435 1440
Asn Leu Ala Gly Ser Pro Lys Asp Val Lys Pro Ala Glu Pro Arg Lys		
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Leu Gly Val Ser Ser Glu Gln Gln Glu Lys Gly Lys Ser Gly Pro Asp		
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Glu Glu Met Met Glu Glu Lys Leu Lys Ser Leu Phe Glu Asp Ile Gln		
1475	1480	1485
Leu Glu Glu Gly Val Glu Ser Glu Glu Met Thr Glu Glu Lys Val Gln		
1490	1495	1500
Ala Ile Leu Lys Arg Val Gln Gln Ala Glu Leu Glu Met Ser Ser Ile		
1505	1510	1515 1520
Thr Gly Trp Gln Asn Glu Thr Ser Ser Gly Asn Leu Glu Ser Cys Ala		
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Gln	Ala	Arg	Val	Thr	Gly	Gly	Leu	Asp	Arg	Leu	Asp	Ser			
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Pro	Asp	Gln	Cys	Arg	Asp	Ser	Ile	Thr	Ser	Tyr	Leu	Lys	Gly	Glu	Ala
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Gly	Lys	Phe	Glu	Ala	Asn	Gly	Ser	His	Thr	Glu	Ile	Thr	Pro	Glu	Ala
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Lys	Thr	Lys	Ser	Tyr	Phe	Pro	Glu	Ser	Gln	Asn	Asp	Val	Gly	Lys	Gln
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Ser	Thr	Lys	Glu	Thr	Leu	Lys	Pro	Lys	Ile	His	Gly	Ser	Gly	His	Val
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Thr	Ser	Lys	Leu	Ile	Ile	Glu	Glu	Thr	Lys	Pro	Cys	Val	Pro	Asp	Leu
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- 46 -

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Lys Asp

<210> 46
<211> 1337
<212> DNA
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<400> 46
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Asp Lys Asp Asn Gln Ala Gln Thr Gln Ala Ile Ala Ala Gly Thr Thr
50 55 60
Thr Thr Ala Ile Gly Thr Ser Thr Thr Cys Pro Ala Asn Gln Met Val
65 70 75 80
Asn Asn Asn Glu Asn Thr Gly Ser Leu Ser Pro Ser Ser Gly Val Gly
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Tyr	Pro	Asn	Asp	Leu	Ala	Lys	Lys	Met	Thr	Lys	Cys	Ser	Lys	Ser	His
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Leu	Pro	Ser	Gln	Gly	Pro	Val	Ile	Ile	Asp	Cys	Arg	Pro	Phe	Met	Glu
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Tyr	Asn	Lys	Ser	His	Ile	Gln	Gly	Ala	Val	His	Ile	Asn	Cys	Ala	Asp
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<213> Homo Sapien
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<211> 904
 <212> PRT
 <213> Homo Sapien

<400> 49

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Phe	Glu	Asp	Glu	Ser	Glu	Gly	Leu	Leu	Gly	Thr	Glu	Gly	Pro	Leu	Glu
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 Leu Val Asp Lys Ala Arg Gln Ile Asn Ile His Asn Leu Ser Ala Phe
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<210> 50
 <211> 2815
 <212> DNA
 <213> Homo Sapien

<400> 50

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<400> 51

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Lys	Tyr	Gly	Tyr	Leu	Phe	Ile	Ser	Val	Leu	Val	Asn	Ser	Asn	Ser	Glu
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		195					200					205			
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		210				215						220			
Val	Pro	Ala	Pro	Trp	Leu	Ser	Val	Lys	Leu	Leu	Arg	Leu	Leu	Gln	Cys
225					230					235					240
Tyr	Pro	Pro	Pro	Glu	Asp	Ala	Ala	Val	Lys	Gly	Arg	Leu	Val	Glu	Cys
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gctcctctag	cccggccacg	gctccgctgc	gggccaccca	ggattactcg	cgtctggctc	300
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Lys	Ser	Gly 210	Phe	Arg	Val	Pro 215	Ser	Ala	Thr	Cys	Gln 220	Pro	Phe	Thr	Pro
Arg 225	Thr	Gly	Ser	Pro	Ser 230	Ser	Ser	Ala	Ser	Ala 235	Cys	Ser	Pro	Gly	Gly
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Pro	Pro	Ala 355	Gly	Met	Thr	Tyr	Pro 360	Gly	Ser	Leu	Ala	Gly 365	Ala	Tyr	Ala
Gly	Tyr 370	Pro	Pro	Gln	Phe 375	Leu	Pro	His	Gly	Val	Ala 380	Leu	Asp	Pro	Thr
Lys 385	Pro	Gly	Ser	Leu	Val 390	Gly	Ala	Gln	Leu	Ala 395	Ala	Ala	Ala	Ala	Gly
Ser	Leu	Gly	Cys 405	Ser	Lys	Pro	Ala	Gly	Ser	Ser 410	Pro	Leu	Ala	Gly	Ala
Ser	Pro	Pro 420	Ser	Val	Met	Thr	Ala 425	Ser	Leu	Cys	Arg	Asp 430	Pro	Tyr	Cys
Leu	Ser	Tyr 435	His	Cys	Ala	Ser	His 440	Leu	Ala	Gly	Ala 445	Ala	Ala	Ala	Ser
Ala	Ser	Cys 450	Ala	His	Asp	Pro 455	Ala	Ala	Ala	Ala 460	Ala	Ala	Ala	Leu	Ser
Gly 465	Tyr	Pro	Leu	Val	Tyr 470	Pro	Thr	His	Pro	Leu 475	His	Gly	Val	His	Ser
Ser	Leu	Thr	Ala 485	Ala	Ala	Ala	Ala	Gly	Ala 490	Thr	Pro	Pro	Ser	Leu	Ala
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Pro	His	Ile 515	Cys	Asn	Trp	Val	Ser 520	Ala	Asn	Gly	Pro	Cys 525	Asp	Lys	Arg
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Leu	Ala	Ser	Ala 565	Ala	Ala	Ala	Ala	Met	Ala 570	Cys	His	Met	His	Ile	Pro

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Pro	Tyr	Tyr	Ser	Pro	Tyr	Ala	Leu	Tyr	Gly	Gln	Arg	Leu	Thr	Thr	Ala
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Table 1: Genetic modifiers

modifier	flyCT	Start	End	hCG	hCT	hCP	Start	End	E-value	gene name / protein family	comments	SEQ ID NO (hCThCP)
EP(2)2107	CT25384	94	183	hCG37225	hCT28457	hCP47994	96	185	4.00E-32	TG-interacting factor / TALEKNOX homeobox protein	modifier of Dps and C99	67
EP(2)2122	CT11970	54	1411	hCG32190	hCT13283	hCP39677	12	348	4.00E-75	n/a	modifier of Dps and C99	89
EP(2)2151	CT3996	27	392	hCG32926	hCT14025	hCP40373	39	415	1.00E-109	NAP1 / aspartyl protease-related	modifier of C99	10/11
EP(2)2162	CT7676	15	374	hCG30594	hCT21765	hCP44907	13	373	3.00E-97	n/a	modifier of Dps and C99, lethal over C99	12/13
EP(2)2173	CT14619	10	531	hCG23983	hCT15097	hCP41313	100	564	1.00E-25	Drosophila noca Zn finger transcription factor ortholog	modifier of Dps and C99, human ortholog on 10q	14/15, 16/17, 52/53
EP(2)2205	CT9828	93	619	hCG41821	hCT33094	hCP51674	668	1180	4.00E-66	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1 (ACE)	modifier of Dps and C99, metalloprotease	18/19
EP(2)2511	CT11457	6	258	hCG20663	hCT11743	hCP38288	28	2,78E+02	2.00E-65	copper chaperone for superoxide dismutase / superoxide dismutase [Cu-Zn]	modifier of Dps and C99	20/21
EP(2)2554	CT10410	6	192	hCG39955	hCT31207	hCP49745	5	198	2.00E-16	glutathione S-transferase theta 1	modifier of Dps and C99	22/23
EP(2)2554	CT10310	15	661	hCG40293	hCT31548	hCP50060	18	617	2.00E-90	intersectin-related	modifier of Dps and C99	24/25
EP(3)3041	CT5335	14	227	hCG42003	hCT33279	hCP51813	29	246	1.00E-39	HSA011916	modifier of Dps and C99	26/27
EP(X)1526	CT10709	7	597	hCG37950	hCT29186	hCP47880	5	519	1.00E-168	protein kinase inhibitor P58-related	modifier of Dps and C99	28/29
P1396=[(2)05206	CT13013	316	655	hCG20435	hCT11514	hCP38090	106	404	2.00E-72	cyclin	modifier of Dps and C99	30/31
P1486=[(3)00090	CT22943	1818	2491	hCG32338	hCT23526	hCP46544	663	1248	2.00E-84	retinoblastoma binding protein-related	modifier of Dps and C99	32/33
P1505=[(3)00643	CT23724	760	1123	hCG40234	hCT31488	hCP50765	131	439	3.00E-63	early growth response 2 (Krox-20 (Drosophila) homolog)	modifier of Dps, human ortholog on 10q	34/35
P1548=[(3)01814	CT24038	75	167	hCG18539	hCT9598	hCP36359	1	93	1.00E-31	n/a	modifier of Dps and C99	36/37
P2093=[(3)05C8	CT18339	218	438	hCG14845	hCT5866	hCP35211	38	278	6.00E-31	baculoviral IAP repeat-containing 4 / apoptosis inhibitor related	modifier of Dps and C99	38/39
P2093=[(3)05C8	CT18415	62	293	hCG17907	hCT8961	hCP33787	353	569	2.00E-18	ankyrin-related	modifier of Dps, human homolog on 10q	40/41
P2093=[(3)05C8	CT18415	50	349	hCG41783	hCT33056	hCP51594	7	307	2.00E-23	ankyrin-3, ankyrin-G	modifier of Dps, human homolog on 10q	42/43
P2104=[(3)13B3	CT13750	372	733	hCG201263	hCT201265	hCP201588	61	432	1.00E-111	ubiquitin carboxy-terminal hydrolase	modifier of Dps and C99	44/45
P2121=[(3)4E1	CT23760	87	283	hCG25031	hCT16153	hCP41935	239	437	2.00E-37	dual specificity protein phosphatase	modifier of Dps and C99	46/47
P2122=[(3)14074	CT23073	5	879	hCG39269	hCT30519	hCP50592	21	902	0	minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin) / DNA replication licensing factor MCM	modifier of Dps and C99	48/49
P2319=[(2)06694	CT13966	1	932	hCG21123	hCT12209	hCP38695	18	937	0	alpha-adaptin	modifier of C99	50/51